I claim:

1. A recombinagenic composition comprising

a single stranded oligonucleotide having a sequence that forms a triple stranded nucleic acid molecule with a target sequence double stranded nucleic acid molecule,

a carrier suitable for administration to human or animal cells of an effective amount of the single stranded oligonucleotide for targeted recombination of the double stranded nucleic acid molecule, the single-stranded oligonucleotide having a sequence that forms a triple-stranded nucleic acid molecule with a target sequence of the double stranded nucleic acid molecule and a Kd of less than 2×10^{-6},

wherein recombination of a donor nucleic acid into the target sequence, induced by triple helix formation between the single stranded oligonucleotide and double stranded nucleic acid molecule, will activate, inactivate, or alter the activity or function of the double-stranded nucleic molecule or the protein it encodes.

2. The recombinagenic composition of claim 1 wherein the donor nucleic acid is single stranded or double stranded.

3. The composition of claim 1 wherein the oligonucleotide is between 10 and 60 nucleotides residues in length.

4. The composition of claim 1 wherein the donor nucleic acid is tethered to the single stranded oligonucleotide.

5. The composition of claim 1 wherein the double-stranded nucleic acid

molecule encodes a biologically active protein and the targeted recombination alters the activity of the protein.

6. The composition of claim 5 wherein the double-stranded nucleic acid molecule is selected from the group consisting of a gene, an oncogene, a defective gene, a viral genome, and a portion of a viral genome.

7. A method for targeted recombination of a nucleic acid molecule comprising the steps of:

a) hybridizing a single stranded oligonucleotide having a sequence that forms a triple stranded nucleic acid molecule with a target sequence double stranded nucleic acid molecule and a Kd of less than 2×10^{-6}; and

b) recombining a donor nucleic acid into the target sequence, induced by triple helix formation between the single stranded oligonucleotide and double stranded nucleic acid molecule.

8. The method of claim 7, wherein the single stranded oligonucleotide is between 10 and 60 nucleotides in length.

9. The method of claim 7, wherein the single stranded oligonucleotide is tethered to the donor DNA fragment.

10. The method of claim 7 wherein the double stranded nucleic acid molecule encodes a protein and the targeted recombination alters the activity of the protein encoded by the double-stranded nucleic acid molecule.

11. The method of claim 7, wherein the double-stranded nucleic acid molecule is selected from the group consisting of a gene, an oncogene, a defective gene, a viral genome, and a portion of a viral genome.

12. The method of claim 7, wherein the donor fragment is at least 30 nucleotide residues in length.

13. The composition of claim 1, wherein the donor fragment is at least 30 nucleotide residues in length.

14. The composition of claim 4, wherein the tethered donor fragment is at least 4 nucleotides in length.

15. A method to produce heritable changes in the genome of an intact human or animal comprising the steps:

a) injecting an oligonucleotide having a sequence that forms a triple stranded nucleic acid molecule with a target region of the genome, and having a Kd of less than 2×10^{-6},

b) binding the oligonucleotide to the target region, and

c) mutating the target region.

16. The method of claim 15 wherein the oligonucleotide is between 10 and 60 nucleotides in length.

17. The method of claim 15 wherein the oligonucleotide is dissolved in a physiologically acceptable carrier.

18. The method of claim 15 wherein the oligonucleotide is recombinagenic.

19. The method of claim 18 wherein the oligonucleotide stimulates recombination of an exogenously supplied DNA fragment with the target region of the genome.

20. The method of claim 18 wherein the oligonucleotide stimulates

recombination of a tethered DNA fragment with the target region of the genome.

21. The method of claim 15 wherein the target region is selected from the group consisting of a gene, an oncogene, a defective gene, a viral genome, and a portion of a viral genome.

22. The method of claim 21 wherein the gene is a defective β-hemoglobin gene, cystic fibrosis gene, xerderma pigmentosum gene, nucleotide excision repair pathway gene or hemophilia gene.

23. The method of claim 15 wherein the oligonucleotide is composed of homopurine or homopyrimidine nucleotides.

24. The method of claim 15 wherein the oligonucleotide is composed of polypurine or polyrimidine nucleotides.

25. The method of claim 9 wherein the donor fragment is between 10 and 40 nucleotides.